AMENDMENT

In the Specification:

Please amend the specification as follows:

Please replace the paragraphs on page 4, line 35 to page 5, line 18, with the following:

Figure 11. Hydrophilicity amino acid profile of 55P5H4 determined by computer algorithm sequence analysis using the method of Hopp and Woods (Hopp T.P., Woods K.R., 1981. Proc. Natl. Acad. Sci. U.S.A. 78:3824-3828) accessed on the Protscale website at the world wide web address expasy.ch/cgi-bin/protscale.pl through the ExPasy molecular biology server.

Figure 12. Hydropathicity amino acid profile of 55P5H4 determined by computer algorithm sequence analysis using the method of Kyte and Doolittle (Kyte J., Doolittle R.F., 1982. J. Mol. Biol. 157:105-132) accessed on the ProtScale website at the world wide web address expasy.ch/cgi-bin/protscale.pl through the ExPasy molecular biology server.

B1 Figure 13. Percent accessible residues amino acid profile of 55P5H4 determined by computer algorithm sequence analysis using the method of Janin (Janin J., 1979 Nature 277:491-492) accessed on the ProtScale website at the world wide web address expasy.ch/cgi-bin/protscale.pl through the ExPasy molecular biology server.

Figure 14. Average flexibility amino acid profile of 55P5H4 determined by computer algorithm sequence analysis using the method of Bhaskaran and Ponnuswamy (Bhaskaran R., and Ponnuswamy P.K., 1988. Int. J. Pept. Protein Res. 32:242-255) accessed on the ProtScale website at the world wide web address expasy.ch/cgi-bin/protscale.pl through the ExPasy molecular biology server.

Figure 15. Beta-turn amino acid profile of 55P5H4 determined by computer algorithm sequence analysis using the method of Deleage and Roux (Deleage, G., Roux B. 1987 Protein Engineering 1:289-294) accessed on the ProtScale website at the world wide web address expasy.ch/cgi-bin/protscale.pl through the ExPasy molecular biology server.

Please replace the paragraph on page 21, lines 3-10, with the following:

As discussed herein, redundancy in the genetic code permits variation in 55P4H4 gene sequences. In particular, it is known in the art that specific host species often have specific codon preferences, and thus one can adapt the disclosed sequence as preferred for a desired host. For example, preferred analog codon sequences typically have rare codons (i.e., codons having a usage frequency of less than about 20% in known sequences of the desired host) replaced with higher frequency codons. Codon preferences for a specific species are calculated, for example, by utilizing codon usage tables available on the INTERNET such as: at the world wide web address dna.affrc.go.jp/~nakamura/codon.html.

Please replace the paragraphs on page 24, lines 11-24, with the following:

Additional illustrative embodiments of the invention disclosed herein include 55P4H4 polypeptides comprising the amino acid residues of one or more of the biological motifs contained within the 55P4H4 polypeptide sequence set forth in Figure 2 or Figure 3. Various motifs are known in the art, and a protein can be evaluated for the presence of such motifs by a number of publicly available sites (see, e.g.: the world wide web addresses pfam.wustl.edu/; searchlauncher.bcm.tmc.edu/seq-search/struc-predict.html; psort.ims.u-tokyo.ac.jp/; cbs.dtu.dk/; ebi.ac.uk/interpro/scan.html; expasy.ch/tools/scnpsit1.html; Epimatrix™ and Epimer™, Brown University, brown.edu/Research/TB-HIV_Lab/epimatrix/epimatrix.html; and BIMAS, bimas.dcrt.nih.gov/).

Motif bearing subsequences of the 55P4H4 protein are set forth and identified in Table XIX.

Table XX sets forth several frequently occurring motifs based on pfam searches at the world wide web address pfam.wustl.edu/. The columns of Table XX list (1) motif name abbreviation, (2) percent identity found amongst the different member of the motif family, (3) motif name or description and (4) most common function; location information is included if the motif is relevant for location.

Please replace the paragraph on page 25, lines 2-11, with the following:

In another embodiment, proteins of the invention comprise one or more of the immunoreactive epitopes identified in accordance with art-accepted methods, such as the peptides set forth in Tables V-XVIII. CTL epitopes can be determined using specific algorithms to identify peptides within an 55P4H4 protein that are capable of optimally binding to specified HLA alleles (e.g., Table IV (A) and Table IV (B); Epimatrix™ and Epimer™, Brown University, at the world wide web address brown.edu/Research/TB-HIV_Lab/epimatrix/epimatrix.html; and BIMAS, at the world wide web address bimas.dcrt.nih.gov/). Moreover, processes for identifying peptides that have sufficient binding affinity for HLA molecules and which are correlated with being immunogenic epitopes, are well known in the art, and are carried out without undue experimentation. In addition, processes for identifying peptides that are immunogenic epitopes, are well known in the art, and are carried out without undue experimentation either *in vitro* or *in vivo*.

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Please replace the paragraph on page 26, line 19-page 27, line 5, with the following:

CTL epitopes can be determined using specific algorithms to identify peptides within an 55P4H4 protein that are capable of optimally binding to specified HLA alleles (e.g., Table IV (A) and Table IV (B); Epimatrix™ and Epimer™, Brown University at the world wide web addresses brown.edu/Research/TB-HIV_Lab/epimatrix/epimatrix.html); and BIMAS, bimas.dcrt.nih.gov/). Illustrating this, peptide epitopes from 55P4H4 that are presented in the context of human MHC class I molecules HLA-A1, A2, A3, A11, A24, B7 and B35 were predicted (Tables V-XVIII). Specifically, the complete amino acid sequence of the 55P4H4 protein was entered into the HLA Peptide Motif Search algorithm found in the Bioinformatics and Molecular Analysis Section (BIMAS) web site listed above. The HLA peptide motif search algorithm was developed by Dr. Ken Parker based on binding of specific peptide sequences in the groove of HLA Class I molecules and specifically HLA-A2 (see, e.g., Falk et al., Nature 351: 290-6 (1991); Hunt et al., Science 255:1261-3 (1992); Parker et al., J. Immunol. 149:3580-7 (1992); Parker et al., J. Immunol. 152:163-75 (1994)). This algorithm allows location and ranking of 8-mer, 9-mer, and 10-mer peptides from a complete protein sequence for predicted binding to HLA-A2 as well as numerous other HLA Class I molecules. Many HLA class I

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binding peptides are 8-, 9-, 10 or 11-mers. For example, for class I HLA-A2, the epitopes preferably contain a leucine (L) or methionine (M) at position 2 and a valine (V) or leucine (L) at the C-terminus (see, e.g., Parker et al., J. Immunol. 149:3580-7 (1992)). Selected results of 55P4H4 predicted binding peptides are shown in Tables V-XVIII herein. In Tables V-XVIII, the B5 top 50 ranking candidates, 9-mers and 10-mers, for each family member are shown along with their location, the amino acid sequence of each specific peptide, and an estimated binding score. The binding score corresponds to the estimated half-time of dissociation of complexes containing the peptide at 37°C at pH 6.5. Peptides with the highest binding score are predicted to be the most tightly bound to HLA Class I on the cell surface for the greatest period of time and thus represent the best immunogenic targets for T-cell recognition.

Please replace the paragraph on page 45, line 32-page 46, line 5, with the following:

Genetic immunization methods can be employed to generate prophylactic or therapeutic humoral and cellular immune responses directed against cancer cells expressing 55P4H4. Constructs comprising DNA encoding a 55P4H4-related protein/immunogen and appropriate B6 regulatory sequences can be injected directly into muscle or skin of an individual, such that the cells of the muscle or skin take-up the construct and express the encoded 55P4H4 protein/immunogen. Alternatively, a vaccine comprises a 55P4H4-related protein. Expression of the 55P4H4-related protein immunogen results in the generation of prophylactic or therapeutic humoral and cellular immunity against cells that bear 55P4H4 protein. Various prophylactic and therapeutic genetic immunization techniques known in the art can be used (for review, see information and references published at the world wide web address genweb.com).

Please replace the paragraph on page 46, lines 17-34, with the following:

CTL epitopes can be determined using specific algorithms to identify peptides within 55P4H4 protein that are capable of optimally binding to specified HLA alleles (e.g., Table IV (A) and Table IV (B); Epimer™ and Epimatrix™, Brown University at the world wide B7 web addresses brown.edu/Research/TB-HIV_Lab/epimatrix/epimatrix.html; and, BIMAS, bimas.dcrt.nih.gov/). In a preferred embodiment, the 55P4H4 immunogen contains one or more amino acid sequences identified using one of the pertinent analytical techniques well known in

the art, such as the sequences shown in Tables V-XVIII or a peptide of 8, 9, 10 or 11 amino acids specified by an HLA Class I motif (e.g., Table IV (A)) and/or a peptide of at least 9 amino acids that comprises an HLA Class II motif (e.g., Table IV (B)). As is appreciated in the art, the HLA Class I binding groove is essentially closed ended so that peptides of only a particular size range can fit into the groove and be bound, generally HLA Class I epitopes are 8, 9, 10, or 11 amino acids long. In contrast, the HLA Class II binding groove is essentially open ended; therefore a peptide of about 9 or more amino acids can be bound by an HLA Class II molecule. Due to the binding groove differences between HLA Class I and II, HLA Class I motifs are length specific, i.e., position two of a Class I motif is the second amino acid in an amino to carboxyl direction of the peptide. The amino acid positions in a Class II motif are relative only to each other, not the overall peptide, i.e., additional amino acids can be attached to the amino and/or carboxyl termini of a motif-bearing sequence. HLA Class II epitopes are often 9, 10, 11, 12, 13, 14, 15, 16, 17, 18, 19, 20, 21, 22, 23, 24, or 25 amino acids long, or longer than 25 amino acids.

Please replace the paragraph on page 56, lines 18-23, with the following:

Sequence analysis of 55P4H4 reveals homology to a protein that is regulated by hypoxia (PCT/US98/17296, WO 99/09049). The 55P4H4 ORF is 32% identical and 55% homologous to RTP779 over a 180 amino acid region, and 32% identical and 54% homologous to RTP801, the rat orthologue of RTP779 (Fig. 4). 55P4H4 is predicted to be a cytoplasmic protein by PSORT analysis at the world wide web address psort.ims-u-tokyo.ac.jp/form.html with a lower possibility of nuclear or mitochondrial localization.

Please replace the paragraph on page 58, lines 23-28, with the following:

This vector and the mapping program at the world wide web address genome.wi.mit.edu/cgi-bin/contig/rhmapper.pl placed 55P4H4 to chromosome 4q22.3-24. A variety of chromosomal abnormalities in 4q22.3-24 including amplifications have been identified as frequent cytogenetic abnormalities in a number of different cancers. Nilbert et al., 1988, Cancer Genet. Cytogenet. 34(2): 209-218; Yeatman et al., 1996, Clin. Exp. Metastasis 14(3):246-252; and Joos et al., 2000, Cancer Res. 60(3): 549-552.

Please replace the paragraph on page 59, lines 25-27, with the following:

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Figures 11, 12, 13, 14, and 15 depict graphically five amino acid profiles of the 55P5H4 amino acid sequence, each assessment available by accessing the ProtScale website at the world wide web address expasy.ch/cgi-bin/protscale.pl on the ExPasy molecular biology server.

Please replace the paragraph on page 73, lines 20-27, with the following:

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Antibody efficacy on tumor growth and metastasis formation is studied, e.g., in a mouse orthotopic prostate cancer xenograft model. The antibodies can be unconjugated, as discussed in this Example, or can be conjugated to a therapeutic modality, as appreciated in the art. We demonstrate that anti-55P4H4 mAbs inhibit formation of both the androgen-dependent LAPC-9 and androgen-independent PC3-55P4H4 tumor xenografts. Anti-55P4H4 mAbs also retard the growth of established orthotopic tumors and prolonged survival of tumor-bearing mice. These results indicate the utility of anti-55P4H4 mAbs in the treatment of local and advanced stages of prostate cancer. (See, e.g., Saffran, D., et al., PNAS 10:1073-1078 or the world wide web address pnas.org/cgi/doi/10.1073/pnas.051624698.)

Please replace the paragraph on page 74, line 30-page 75, line 5, with the following:

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Subcutaneous (s.c.) tumors are generated by injection of 1 x 10^6 LAPC-9, PC3, or PC3-55P4H4 cells mixed at a 1:1 dilution with Matrigel (Collaborative Research) in the right flank of male SCID mice. To test antibody efficacy on tumor formation, i.p. antibody injections are started on the same day as tumor-cell injections. As a control, mice are injected with either purified mouse IgG (ICN) or PBS; or a purified monoclonal antibody that recognizes an irrelevant antigen not expressed in human cells. In preliminary studies, no difference is found between mouse IgG or PBS on tumor growth. Tumor sizes are determined by vernier caliper measurements, and the tumor volume is calculated as length x width x height. Mice with s.c. tumors greater than 1.5 cm in diameter are sacrificed. PSA levels are determined by using a PSA ELISA kit (Anogen, Mississauga, Ontario). Circulating levels of anti-55P4H4 mAbs are determined by a capture ELISA kit (Bethyl Laboratories, Montgomery, TX). (See, e.g.,

B12 Saffran, D., et al., PNAS 10:1073-1078 or the world wide web address pnas.org/cgi/doi/10.1073/pnas.051624698.)

Please replace the paragraph on page 90, lines 14-16, with the following:

B13 Epitopes are often selected that have a binding affinity of an IC50 of 500 nM or less for an HLA class I molecule, or for class II, an IC50 of 1000 nM or less; or HLA Class I peptides with high binding scores form the BIMAS web site at the world wide web address bimas.dcrt.nih.gov/.

In the Claims:

Please replace the presently pending claims with the following claims:

Please cancel claims 56-65.

66. (Amended) An isolated 55P4H4-related protein that comprises an amino acid sequence encoded by a polynucleotide selected from the group consisting of:

(a) a polynucleotide consisting of the sequence as shown in SEQ ID NO: 1;

(b) a polynucleotide consisting of the sequence as shown in SEQ ID NO: 1, from nucleotide residue number 204 through nucleotide residue number 782;

B14 (c) a polynucleotide that is the cDNA contained in the plasmid designated p55P4H4-EBB12 deposited with American Type Culture Collection as Accession No. PTA-1894;

(d) a polynucleotide that encodes a 55P4H4-related protein that is at least 90% homologous to the entire amino acid sequence shown in SEQ ID NO: 2 and which is specifically bound by an antibody that specifically binds the protein of SEQ. ID. No.: 2; and

(e) a polynucleotide that encodes a fragment containing at least 30 contiguous amino acids of SEQ ID NO: 2 and which is specifically bound by an antibody that specifically binds the protein of SEQ. ID. No.: 2.

Please cancel claims 67-69.